

1

SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> D6-acetylenase and D6-desaturase from Ceratodon
purpureus

<130> 99 1388

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<150> 19925718.3

<151> 1999-06-07

<160> 12

<170> PatentIn Vers. 2.0

<210> 1

<211> 2040

<212> DNA

<213> Ceratodon purpureus

<220>

<221> CDS

<222> (176)..(1627)

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tcagggtcga tcaggttatt ctgaaaaagg ctgcgtctgt gagcagtttgc aaaaa atg 178

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1

gcc ctc gtt acc gac ttt ctg aac ttt ctg ggc acg aca tgg agc aag 226

Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr Trp Ser Lys

5

10

15

tac agc gtg tac acc cat agc tat gct gga aac tat ggg cct act ttg 274

Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly Pro Thr Leu

20

25

30

aag cac gcc aaa aag gtt tct gct caa ggt aaa act gcg gga cag aca 322

Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala Gly Gln Thr

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45

ctg aga cag aga tcg gtg cag gac aaa aag cca ggc act tac tct ctg 370

Leu Arg Gln Arg Ser Val Gln Asp Lys Pro Gly Thr Tyr Ser Leu

50

55

60

65

gcc gat gtt gct tct cac gac agg cct gga gac tgc tgg atg atc gtc 418
 Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp Met Ile Val
 70 75 80

aaa gag aag gtg tat gat att agc cgt ttt gcg gac gac cac cct gga 466
 Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp His Pro Gly
 85 90 95

ggg acg gta att agc acc tac ttt ggg cggtt gat ggc aca gac gtt ttc 514
 Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe
 100 105 110

gca aca ttc cat cca cct gcc gca tgg aag caa ctc aat gac tac tac 562
 Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn Asp Tyr Tyr
 115 120 125

att gga gac ctt gct agg gaa gag ccc ctt gat gaa ttg ctt aaa gac 610
 Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu Leu Lys Asp
 130 135 140 145

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 Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu Phe Lys Ser
 150 155 160

tcc aag gcc tgg ttc ctg ctt cag act ctg att aat gca gct ctc ttt 706
 Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala Ala Leu Phe
 165 170 175

gct gcg agc att gcg act atc tgt tac gac aag agt tac tgg gct att 754
 Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr Trp Ala Ile
 180 185 190

gtg ctg tca gcc agt ttg atg ggt ctc ttc gtc caa cag tgt gga tgg 802
 Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln Cys Gly Trp
 195 200 205

ctt gcc cat gat ttc ctt cat caa cag gtc ttt gag aac cgt acc gcg 850
 Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn Arg Thr Ala
 210 215 220 225

aac tcc ttc ttt ggc tat ttg ttc ggc aat tgc gtg ctt ggc ttt agt 898
 Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu Gly Phe Ser
 230 235 240

gta tca tgg tgg agg acg aag cac aac att cat cat act gct ccg aat 946
 Val Ser Trp Trp Arg Thr Lys His Asn Ile His His Thr Ala Pro Asn
 245 250 255

gag tgc gac gaa cag tac aca cct cta gac gaa gac att gat act ctc 994

Glu	Cys	Asp	Glu	Gln	Tyr	Thr	Pro	Leu	Asp	Glu	Asp	Ile	Asp	Thr	Leu	
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ccc atc att gcc tgg agc aag gaa att ttg gcc acc gtt gag agc aag															1042	
Pro	Ile	Ile	Ala	Trp	Ser	Lys	Glu	Ile	Leu	Ala	Thr	Val	Glu	Ser	Lys	
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aga att ttg cga gtg ctt caa tat cag cac tac atg att ctg cct cta															1090	
Arg	Ile	Leu	Arg	Val	Leu	Gln	Tyr	Gln	His	Tyr	Met	Ile	Leu	Pro	Leu	
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Leu	Phe	Met	Ala	Arg	Tyr	Ser	Trp	Thr	Phe	Gly	Ser	Leu	Leu	Phe	Thr	
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Val	Ala	Phe	His	Tyr	Ala	Trp	Phe	Ser	Trp	Ala	Ala	Phe	His	Ile	Leu	
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ccg ggt gtc gct aag cct ctt gcg tgg atg gta gca act gag ctt gtg															1282	
Pro	Gly	Val	Ala	Lys	Pro	Leu	Ala	Trp	Met	Val	Ala	Thr	Glu	Leu	Val	
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gcc ggt ttg ttg gga ttc gtg ttt acg ttg agt cac aat gga aag															1330	
Ala	Gly	Leu	Leu	Leu	Gly	Phe	Val	Phe	Thr	Leu	Ser	His	Asn	Gly	Lys	
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Glu	Val	Tyr	Asn	Glu	Ser	Lys	Asp	Phe	Val	Arg	Ala	Gln	Val	Ile	Thr	
390				395						400						
acc cgt aac acc aag cga ggc tgg ttc aac gat tgg ttc act ggg gga															1426	
Thr	Arg	Asn	Thr	Lys	Arg	Gly	Trp	Phe	Asn	Asp	Trp	Phe	Thr	Gly	Gly	
405				410					415							
ctc gac acc cag att gag cat cac ctg ttt cca aca atg ccc agg cac															1474	
Leu	Asp	Thr	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Thr	Met	Pro	Arg	His	
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aac tac ccc aag atc gca cct cag gtc gag gct ctt tgc aag aag cac															1522	
Asn	Tyr	Pro	Lys	Ile	Ala	Pro	Gln	Val	Glu	Ala	Leu	Cys	Lys	His		
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ggc ctc gag tac gat aat gtc tcc gtc gtt ggt gcc tct gtc gcg gtt															1570	
Gly	Leu	Glu	Tyr	Asp	Asn	Val	Ser	Val	Val	Gly	Ala	Ser	Val	Ala	Val	
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 Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile Arg Leu His
 470 475 480

gct cac taa gaaatcgctcg aactttgact attcattttt ttgcgcctggc 1667
 Ala His

tacctcaaata gttcgggagc aggtgcttgg cagtgtgttc aaccggagcg cactgaaaat 1727

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atatatgaaa ctttttgat gcaacaagta gcattcaatt gaagacattt ttcgagat 1847

aattcgcagt gtttctattt agcgggcata cgtactagtc catatcggcg gttgccgaga 1907

gtttacatta ttagttggca caacgagtag atctagtgtt aatttctatt tccgcattgt 1967

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<211> 483

<212> PRT

<213> Ceratodon purpureus

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 35 40 45

Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr Tyr Ser
 50 55 60

Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp Met Ile
 65 70 75 80

Val Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp His Pro
 85 90 95

Gly Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val
 100 105 110

Phe Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn Asp Tyr
 115 120 125

Tyr Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu Leu Lys
130 135 140

Asp Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu Phe Lys
145 150 155 160

Ser Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala Ala Leu
165 170 175

Phe Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr Trp Ala
180 185 190

Ile Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln Cys Gly
195 200 205

Trp Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn Arg Thr
210 215 220

Ala Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu Gly Phe
225 230 235 240

Ser Val Ser Trp Trp Arg Thr Lys His Asn Ile His His Thr Ala Pro
245 250 255

Asn Glu Cys Asp Glu Gln Tyr Thr Pro Leu Asp Glu Asp Ile Asp Thr
260 265 270

Leu Pro Ile Ile Ala Trp Ser Lys Glu Ile Leu Ala Thr Val Glu Ser
275 280 285

Lys Arg Ile Leu Arg Val Leu Gln Tyr Gln His Tyr Met Ile Leu Pro
290 295 300

Leu Leu Phe Met Ala Arg Tyr Ser Trp Thr Phe Gly Ser Leu Leu Phe
305 310 315 320

Thr Phe Asn Pro Asp Leu Ser Thr Thr Lys Gly Leu Ile Glu Lys Gly
325 330 335

Thr Val Ala Phe His Tyr Ala Trp Phe Ser Trp Ala Ala Phe His Ile
340 345 350

Leu Pro Gly Val Ala Lys Pro Leu Ala Trp Met Val Ala Thr Glu Leu
355 360 365

Val Ala Gly Leu Leu Leu Gly Phe Val Phe Thr Leu Ser His Asn Gly
370 375 380

Lys Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln Val Ile
385 390 395 400

Thr Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe Thr Gly
 405 410 415

Gly Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg
 420 425 430

His Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys
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His Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser Val Ala
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<213> Ceratodon purpureus

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tgg agc aag tac agc gtg tac acc cat agc tat gct gga aac tat ggg 99
 Trp Ser Lys Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly
 15 20 25 30

cct act ttg aag cac gcc aaa aag gtt tct gct caa ggt aaa act gcg 147
 Pro Thr Leu Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala
 35 40 45

gga cag aca ctg aga cag aga tcg gtg cag gac aaa aag cca ggc act 195
 Gly Gln Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr
 50 55 60

tac tct ctg gcc gat gtt gct tct cac gac agg cct gga gac tgc tgg 243
 Tyr Ser Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp
 65 70 75

atg atc gtc aaa gag aag gtg tat gat att agc cgt ttt gcg gac gac 291
 Met Ile Val Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp

80	85	90	
cac cct gga ggg acg gta att agc acc tac ttt ggg cg ^g gat ggc aca			339
His Pro Gly Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr			
95	100	105	110
gac gtt ttc gca aca ttc cat cca cct gcc gca tgg aag caa ctc aat			387
Asp Val Phe Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn			
115	120	125	
gac tac tac att gga gac ctt gct agg gaa gag ccc ctt gat gaa ttg			435
Asp Tyr Tyr Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu			
130	135	140	
ctt aaa gac tac aga gat atg aga gcc gag ttt gtt aga gaa ggg ctt			483
Leu Lys Asp Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu			
145	150	155	
ttc aag agt tcc aag gcc tgg ttc ctg ctt cag act ctg att aat gca			531
Phe Lys Ser Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala			
160	165	170	
gct ctc ttt gct gc ^g agc att gc ^g act atc tgt tac gac aag agt tac			579
Ala Leu Phe Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr			
175	180	185	190
tgg gct att gtg ctg tca gcc agt ttg atg ggt ctc ttc gtc caa cag			627
Trp Ala Ile Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln			
195	200	205	
tgt gga tgg ctt gcc cat gat ttc ctt cat caa cag gtc ttt gag aac			675
Cys Gly Trp Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn			
210	215	220	
cgt acc gc ^g aac tcc ttc ttt ggc tat ttg ttc ggc aat tgc gtg ctt			723
Arg Thr Ala Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu			
225	230	235	
ggc ttt agt gta tca tgg tgg agg acg aag cac aac att cat cat act			771
Gly Phe Ser Val Ser Trp Trp Arg Thr Lys His Asn Ile His His Thr			
240	245	250	
gct ccg aat gag tgc gac gaa cag tac aca cct cta gac gaa gac att			819
Ala Pro Asn Glu Cys Asp Glu Gln Tyr Thr Pro Leu Asp Glu Asp Ile			
255	260	265	270
gat act ctc ccc atc att gcc tgg agc aag gaa att ttg gcc acc gtt			867
Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Glu Ile Leu Ala Thr Val			
275	280	285	
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35 40 45
Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr Tyr Ser
50 55 60
Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp Met Ile
65 70 75 80
Val Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp His Pro
85 90 95
Gly Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val
100 105 110
Phe Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn Asp Tyr
115 120 125
Tyr Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu Leu Lys
130 135 140
Asp Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu Phe Lys
145 150 155 160
Ser Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala Ala Leu
165 170 175
Phe Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr Trp Ala
180 185 190
Ile Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln Cys Gly
195 200 205
Trp Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn Arg Thr
210 215 220
Ala Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu Gly Phe
225 230 235 240

Ser Val Ser Trp Trp Arg Thr Lys His Asn Ile His His Thr Ala Pro
 245 250 255
 Asn Glu Cys Asp Glu Gln Tyr Thr Pro Leu Asp Glu Asp Ile Asp Thr
 260 265 270
 Leu Pro Ile Ile Ala Trp Ser Lys Glu Ile Leu Ala Thr Val Glu Ser
 275 280 285
 Lys Arg Ile Leu Arg Val Leu Gln Tyr Gln His Tyr Met Ile Leu Pro
 290 295 300
 Leu Leu Phe Met Ala Arg Tyr Ser Trp Thr Phe Gly Ser Leu Leu Phe
 305 310 315 320
 Thr Phe Asn Pro Asp Leu Ser Thr Thr Lys Gly Leu Ile Glu Lys Gly
 325 330 335
 Thr Val Ala Phe His Tyr Ala Trp Phe Ser Trp Ala Ala Phe His Ile
 340 345 350
 Leu Pro Gly Val Ala Lys Pro Leu Ala Trp Met Val Ala Thr Glu Leu
 355 360 365
 Val Ala Gly Leu Leu Leu Gly Phe Val Phe Thr Leu Ser His Asn Gly
 370 375 380
 Lys Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln Val Ile
 385 390 395 400
 Thr Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe Thr Gly
 405 410 415
 Gly Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg
 420 425 430
 His Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys
 435 440 445
 His Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser Val Ala
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<212> DNA

<213> Ceratodon purpureus

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 aattttgcga gtgcttcgat atcagcacta catgattctg cctctattgt tcatggcccg 180
 gtacagttgg acttttggaa gtttgctctt cacattcaat cctgatttgaa gcacgaccaa 240
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 ccatattttg ccgggtgtcg ctaaggctct tgctggatg gtagcaactg agcttgtggc 360
 cggtttgttg ttgggattcg tgtttacgtt gagtcacaat gaaaggagg tttacaatga 420
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															20
															25
															30

Leu	Ala	Thr	Val	Glu	Ser	Lys	Arg	Ile	Leu	Arg	Val	Leu	Gln	Tyr	Gln
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															40
															45

His	Tyr	Met	Ile	Leu	Pro	Leu	Leu	Phe	Met	Ala	Arg	Tyr	Ser	Trp	Thr
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															55
															60

Phe	Gly	Ser	Leu	Leu	Phe	Thr	Phe	Asn	Pro	Asp	Leu	Ser	Thr	Thr	Lys
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															70
															75
															80

Gly	Leu	Ile	Glu	Lys	Gly	Thr	Val	Ala	Phe	His	Tyr	Ala	Trp	Phe	Ser
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															90
															95

Trp	Ala	Ala	Phe	His	Ile	Leu	Pro	Gly	Val	Ala	Lys	Pro	Leu	Ala	Trp
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															105
															110

Met	Val	Ala	Thr	Glu	Leu	Val	Ala	Gly	Leu	Leu	Gly	Phe	Val	Phe
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12

115 120 125

Thr Leu Ser His Asn Gly Lys Glu Val Tyr Asn Glu Ser Lys Asp Phe
 130 135 140

Val Arg Ala Gln Val Ile Thr Thr Arg Asn Thr Lys Arg Gly Trp Phe
 145 150 155 160

Asn Asp Trp Phe Thr Gly Gly Leu Asp Thr Gln Ile Glu
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<212> DNA

<213> Ceratodon purpureus

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ggcgagttgg ctattttggc ggcggccctt cactctcagg cccgagttgc cccttggcga 240

gaagcttttgc gagaggggaa cgatggctttt gcactacattt tggtttaata gtgttgcgtt 300

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tttcctgctc ggatacgtat ttgtacttcag tcacaatggc atggaggtgtt acaatacg 420

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<213> Ceratodon purpureus

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 20 25 30

Leu Ala Thr Val Glu Ser Lys Thr Met Leu Arg Val Leu Gln Tyr Gln
 35 40 45

His	Leu	Phe	Phe	Leu	Val	Leu	Leu	Thr	Phe	Ala	Arg	Ala	Ser	Trp	Leu
50															60
Phe	Trp	Ser	Ala	Ala	Phe	Thr	Leu	Arg	Pro	Glu	Leu	Thr	Leu	Gly	Glu
65															80
Lys	Leu	Leu	Glu	Arg	Gly	Thr	Met	Ala	Leu	His	Tyr	Ile	Trp	Phe	Asn
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Ser	Val	Ala	Phe	Tyr	Leu	Leu	Pro	Gly	Trp	Lys	Pro	Val	Val	Trp	Met
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Val	Val	Ser	Glu	Leu	Met	Ser	Gly	Phe	Leu	Leu	Gly	Tyr	Val	Phe	Val
															125
Leu	Ser	His	Asn	Gly	Met	Glu	Val	Tyr	Asn	Thr	Ser	Lys	Asp	Phe	Val
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Asn	Ala	Gln	Ile	Ala	Ser	Thr	Arg	Asp	Ile	Lys	Ala	Gly	Val	Phe	Asn
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Asp	Trp	Phe	Thr	Gly	Gly	Leu	Asn	Arg	Gln	Ile	Glu				
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aatggctgtt gctcgggtga acctctttgc ccaatccctt ctagtactga cctcgaagaa 240

gcatgtgcca gacaggtggc ttgagctcggt tgctatcggt ttcttctacc tgtggttctt 300

caccctcttg tcgtacactgc ccactgcacc ggagaggctt gcttcgtcc ttgtcagttt 360

tgcagtgaca gggatccagc atgtacagtt ttgcctgaac cacttctcat cgccgggtta 420

tctaggacag ccgaagagca aggcttgggt tgaatctcaa gcacggggca ctctcaatct 480

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Ser Tyr Phe Tyr Glu Arg Val Met Pro Phe Asp Gly Val Ala Arg Ser
35 40 45

Leu Ile Ala Tyr Gln His Trp Thr Phe Tyr Pro Ile Met Ala Val Ala
50 55 60

Arg Val Asn Leu Phe Ala Gln Ser Leu Leu Val Leu Thr Ser Lys Lys
65 70 75 80

His Val Pro Asp Arg Trp Leu Glu Leu Gly Ala Ile Gly Phe Phe Tyr
85 90 95

Leu Trp Phe Phe Thr Leu Leu Ser Tyr Leu Pro Thr Ala Pro Glu Arg
100 105 110

Leu Ala Phe Val Leu Val Ser Phe Ala Val Thr Gly Ile Gln His Val
115 120 125

Gln Phe Cys Leu Asn His Phe Ser Ser Pro Val Tyr Leu Gly Gln Pro
130 135 140

Lys Ser Lys Ala Trp Val Glu Ser Gln Ala Arg Gly Thr Leu Asn Leu
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 ttgtgcgtgtt gtaatcttcg ccggcaga atg gtg tcc cag ggc ggc 176
 Met Val Ser Gln Gly Gly
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ggt ctc tcg cag ggt tcc att gaa gaa aac att gac gtt gag cac ttg 224
 Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn Ile Asp Val Glu His Leu
 10 15 20

gca acg atg ccc ctc gtc agt gac ttc cta aat gtc ctg gga acg act 272
 Ala Thr Met Pro Leu Val Ser Asp Phe Leu Asn Val Leu Gly Thr Thr
 25 30 35

ttg ggc cag tgg agt ctt tcc act aca ttc gct ttc aag agg ctc acg 320
 Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe Ala Phe Lys Arg Leu Thr
 40 45 50

act aag aaa cac agt tcg gac atc tcg gtg gag gca caa aaa gaa tcg 368
 Thr Lys Lys His Ser Ser Asp Ile Ser Val Glu Ala Gln Lys Glu Ser
 55 60 65 70

gtt gcg cgg ggg cca gtt gag aat att tct caa tcg gtt gcg cag ccc 416
 Val Ala Arg Gly Pro Val Glu Asn Ile Ser Gln Ser Val Ala Gln Pro
 75 80 85

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 Ile Arg Arg Arg Trp Val Gln Asp Lys Lys Pro Val Thr Tyr Ser Leu
 90 95 100

aag gat gta gct tcg cac gat atg ccc cag gac tgc tgg att ata atc 512
 Lys Asp Val Ala Ser His Asp Met Pro Gln Asp Cys Trp Ile Ile Ile
 105 110 115

aaa gag aag gtg tat gat gtg agc acc ttc gct gag cag cac cct gga 560
 Lys Glu Lys Val Tyr Asp Val Ser Thr Phe Ala Glu Gln His Pro Gly
 120 125 130

ggc acg gtt atc aac acc tac ttc gga cga gac gcc aca gat gtt ttc 608
 Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg Asp Ala Thr Asp Val Phe
 135 140 145 150

tct act ttc cac gca tcc acc tca tgg aag att ctt cag aat ttc tac 656
 Ser Thr Phe His Ala Ser Thr Ser Trp Lys Ile Leu Gln Asn Phe Tyr
 155 160 165

atc ggg aac ctt gtt agg gag gag ccg act ttg gag ctg ctg aag gag 704

16

Ile Gly Asn Leu Val Arg Glu Glu Pro Thr Leu Glu Leu Leu Lys Glu			
170	175	180	
tac aga gag ttg aga gcc ctt ttc ttg aga gaa cag ctt ttc aag agt			752
Tyr Arg Glu Leu Arg Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser			
185	190	195	
tcc aaa tcc tac tac ctt ttc aag act ctc ata aat gtt tcc att gtt			800
Ser Lys Ser Tyr Tyr Leu Phe Lys Thr Leu Ile Asn Val Ser Ile Val			
200	205	210	
gcc aca agc att gcg ata atc agt ctg tac aag tct tac cgg gcg gtt			848
Ala Thr Ser Ile Ala Ile Ser Leu Tyr Lys Ser Tyr Arg Ala Val			
215	220	225	230
ctg tta tca gcc agt ttg atg ggc ttg ttt att caa cag tgc gga tgg			896
Leu Leu Ser Ala Ser Leu Met Gly Leu Phe Ile Gln Gln Cys Gly Trp			
235	240	245	
ttg tct cac gat ttt cta cac cat cag gta ttt gag aca cgc tgg ctc			944
Leu Ser His Asp Phe Leu His His Gln Val Phe Glu Thr Arg Trp Leu			
250	255	260	
aat gac gtt gtt ggc tat gtg gtc ggc aac gtt gtt ctg gga ttc agt			992
Asn Asp Val Val Gly Tyr Val Val Gly Asn Val Val Leu Gly Phe Ser			
265	270	275	
gtc tcg tgg tgg aag acc aag cac aac ctg cat cat gct gct ccg aat			1040
Val Ser Trp Trp Lys Thr Lys His Asn Leu His His Ala Ala Pro Asn			
280	285	290	
gaa tgc gac caa aag tac aca ccg att gat gag gat att gat act ctc			1088
Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp Glu Asp Ile Asp Thr Leu			
295	300	305	310
ccc atc att gct tgg agt aaa gat ctc ttg gcc act gtt gag agc aag			1136
Pro Ile Ile Ala Trp Ser Lys Asp Leu Leu Ala Thr Val Glu Ser Lys			
315	320	325	
acc atg ttg cga gtt ctt cag tac cag cac cta ttc ttt ttg gtt ctt			1184
Thr Met Leu Arg Val Leu Gln Tyr Gln His Leu Phe Phe Leu Val Leu			
330	335	340	
ttg acg ttt gcc cgg gcg agt tgg cta ttt ttg agc gcg gcc ttc act			1232
Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe Trp Ser Ala Ala Phe Thr			
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ctc agg ccc gag ttg acc ctt ggc gag aag ctt ttg gag agg gga acg			1280
Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys Leu Leu Glu Arg Gly Thr			
360	365	370	

17

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ccc gga tgg aaa cca gtt gta tgg atg gtg gtc agc gag ctc atg tct Pro Gly Trp Lys Pro Val Val Trp Met Val Val Ser Glu Leu Met Ser 395	400	405		1376
ggt ttc ctg ctg gga tac gta ttt gta ctc agt cac aat gga atg gag Gly Phe Leu Leu Gly Tyr Val Phe Val Leu Ser His Asn Gly Met Glu 410	415	420		1424
gtg tac aat acg tca aag gac ttc gtg aat gcc cag att gca tcg act Val Tyr Asn Thr Ser Lys Asp Phe Val Asn Ala Gln Ile Ala Ser Thr 425	430	435		1472
cgc gac atc aaa gca ggg gtg ttt aat gat tgg ttc acc gga ggt ctc Arg Asp Ile Lys Ala Gly Val Phe Asn Asp Trp Phe Thr Gly Gly Leu 440	445	450		1520
aac aga cag att gag cat cat cta ttt cca acg atg ccc agg cac aac Asn Arg Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn 455	460	465	470	1568
ctt aat aaa att tct cct cac gtg gag act ttg tgc aag aag cat gga Leu Asn Lys Ile Ser Pro His Val Glu Thr Leu Cys Lys Lys His Gly 475	480	485		1616
ctg gtc tac gaa gac gtg agc atg gct tcg ggc act tac cgg gtt ttg Leu Val Tyr Glu Asp Val Ser Met Ala Ser Gly Thr Tyr Arg Val Leu 490	495	500		1664
aaa aca ctt aag gac gtt gcc gat gct gct tca cac cag cag ctt gct Lys Thr Leu Lys Asp Val Ala Asp Ala Ala Ser His Gln Gln Leu Ala 505	510	515		1712
gcg agt tga ggcatcgac cactcgatc aacatgggt tctgttatag Ala Ser 520				1761
tgttcatatg tgatcgaggg gaaaaagggtcc catgctctga tctattcttc tggtagccaaat atttttcaat tggaaaggagg ttccctcaattt atcttccatc tatcggttgc catcctgcatt cagagtttagc gttggagtagaa tgttaaggcac ttgttagatata tgcccacat ctgttcgggtt acaatcggtt gattccatgc tattccatcggtt gttcatctcg ttgttataag caagctgaa aaaacatgct acgagattgg cagacgttgtt cttggcagct gtagaggttg gttccattca ttgtgttagta cagaactctc tttatccctgt ttctctacat tacttggat				1821 1881 1941 2001 2061 2121

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2160

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Asn	Val	Leu	Gly	Thr	Thr	Leu	Gly	Gln	Trp	Ser	Leu	Ser	Thr	Thr	Phe
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Ala	Phe	Lys	Arg	Leu	Thr	Thr	Lys	Lys	His	Ser	Ser	Asp	Ile	Ser	Val
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Glu	Ala	Gln	Lys	Glu	Ser	Val	Ala	Arg	Gly	Pro	Val	Glu	Asn	Ile	Ser
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Gln	Ser	Val	Ala	Gln	Pro	Ile	Arg	Arg	Trp	Val	Gln	Asp	Lys	Lys	
												85			95

Pro	Val	Thr	Tyr	Ser	Leu	Lys	Asp	Val	Ala	Ser	His	Asp	Met	Pro	Gln
												100			110

Asp	Cys	Trp	Ile	Ile	Lys	Glu	Lys	Val	Tyr	Asp	Val	Ser	Thr	Phe	
												115			125

Ala	Glu	Gln	His	Pro	Gly	Gly	Thr	Val	Ile	Asn	Thr	Tyr	Phe	Gly	Arg
												130			140

Asp	Ala	Thr	Asp	Val	Phe	Ser	Thr	Phe	His	Ala	Ser	Thr	Ser	Trp	Lys
												145			160

Ile	Leu	Gln	Asn	Phe	Tyr	Ile	Gly	Asn	Leu	Val	Arg	Glu	Glu	Pro	Thr
												165			175

Leu	Glu	Leu	Lys	Glu	Tyr	Arg	Glu	Leu	Arg	Ala	Leu	Phe	Leu	Arg	
												180			190

Glu	Gln	Leu	Phe	Lys	Ser	Ser	Lys	Ser	Tyr	Tyr	Leu	Phe	Lys	Thr	Leu
												195			205

Ile	Asn	Val	Ser	Ile	Val	Ala	Thr	Ser	Ile	Ala	Ile	Ile	Ser	Leu	Tyr
												210			220

Lys Ser Tyr Arg Ala Val Leu Leu Ser Ala Ser Leu Met Gly Leu Phe
 225 230 235 240
 Ile Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val
 245 250 255
 Phe Glu Thr Arg Trp Leu Asn Asp Val Val Gly Tyr Val Val Gly Asn
 260 265 270
 Val Val Leu Gly Phe Ser Val Ser Trp Trp Lys Thr Lys His Asn Leu
 275 280 285
 His His Ala Ala Pro Asn Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp
 290 295 300
 Glu Asp Ile Asp Thr Leu Pro Ile Ala Trp Ser Lys Asp Leu Leu
 305 310 315 320
 Ala Thr Val Glu Ser Lys Thr Met Leu Arg Val Leu Gln Tyr Gln His
 325 330 335
 Leu Phe Phe Leu Val Leu Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe
 340 345 350
 Trp Ser Ala Ala Phe Thr Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys
 355 360 365
 Leu Leu Glu Arg Gly Thr Met Ala Leu His Tyr Ile Trp Phe Asn Ser
 370 375 380
 Val Ala Phe Tyr Leu Leu Pro Gly Trp Lys Pro Val Val Trp Met Val
 385 390 395 400
 Val Ser Glu Leu Met Ser Gly Phe Leu Leu Gly Tyr Val Phe Val Leu
 405 410 415
 Ser His Asn Gly Met Glu Val Tyr Asn Thr Ser Lys Asp Phe Val Asn
 420 425 430
 Ala Gln Ile Ala Ser Thr Arg Asp Ile Lys Ala Gly Val Phe Asn Asp
 435 440 445
 Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro
 450 455 460
 Thr Met Pro Arg His Asn Leu Asn Lys Ile Ser Pro His Val Glu Thr
 465 470 475 480
 Leu Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Met Ala Ser
 485 490 495

20

Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala
500 505 510

Ser His Gln Gln Leu Ala Ala Ser
515 520